

John J Mackay

List of Publications by Year in descending order

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98
papers

7,764
citations

61857

43
h-index

53109

85
g-index

100
all docs

100
docs citations

100
times ranked

6923
citing authors

#	ARTICLE	IF	CITATIONS
1	Spruce giga-genomes: structurally similar yet distinctive with differentially expanding gene families and rapidly evolving genes. <i>Plant Journal</i> , 2022, 111, 1469-1485.	2.8	17
2	Connecting tree-ring phenotypes, genetic associations and transcriptomics to decipher the genomic architecture of drought adaptation in a widespread conifer. <i>Molecular Ecology</i> , 2021, 30, 3898-3917.	2.0	35
3	Physiological responses of rosewoods (<i>Dalbergia cochinchinensis</i>) and <i>D. oliveri</i> under drought and heat stresses. <i>Ecology and Evolution</i> , 2020, 10, 10872-10885.	0.8	8
4	Reference transcriptomes and comparative analyses of six species in the threatened rosewood genus <i>Dalbergia</i> . <i>Scientific Reports</i> , 2020, 10, 17749.	1.6	20
5	Hydroxyacetophenone defenses in white spruce against spruce budworm. <i>Evolutionary Applications</i> , 2020, 13, 62-75.	1.5	12
6	Multiple Metabolic Innovations and Losses Are Associated with Major Transitions in Land Plant Evolution. <i>Current Biology</i> , 2020, 30, 1783-1800.e11.	1.8	42
7	The large repertoire of conifer NLR resistance genes includes drought responsive and highly diversified RNLs. <i>Scientific Reports</i> , 2019, 9, 11614.	1.6	49
8	Functional Analysis of the PgCesA3 White Spruce Cellulose Synthase Gene Promoter in Secondary Xylem. <i>Frontiers in Plant Science</i> , 2019, 10, 626.	1.7	5
9	Gene copy number variations involved in balsam poplar (<i>Populus balsamifera</i> L.) adaptive variations. <i>Molecular Ecology</i> , 2019, 28, 1476-1490.	2.0	31
10	Genetic control and evolutionary potential of a constitutive resistance mechanism against the spruce budworm (<i>Choristoneura fumiferana</i>) in white spruce (<i>Picea glauca</i>). <i>Heredity</i> , 2018, 121, 142-154.	1.2	12
11	Evolution of the biosynthesis of two hydroxyacetophenones in plants. <i>Plant, Cell and Environment</i> , 2018, 41, 620-629.	2.8	19
12	Expansion of the dehydrin gene family in the Pinaceae is associated with considerable structural diversity and drought-responsive expression. <i>Tree Physiology</i> , 2018, 38, 442-456.	1.4	30
13	Association genetics of acetophenone defence against spruce budworm in mature white spruce. <i>BMC Plant Biology</i> , 2018, 18, 231.	1.6	18
14	A high-resolution reference genetic map positioning 8.8K genes for the conifer white spruce: structural genomics implications and correspondence with physical distance. <i>Plant Journal</i> , 2017, 90, 189-203.	2.8	47
15	Insect herbivory (<i>Choristoneura fumiferana</i> , Tortricidea) underlies tree population structure (<i>Picea</i>) Tj ETQq1 1 0.784314 rgBT ₁₅ /Overlock	1.6	15
16	Gene copy number variations in adaptive evolution: The genomic distribution of gene copy number variations revealed by genetic mapping and their adaptive role in an undomesticated species, white spruce (<i>Picea glauca</i>). <i>Molecular Ecology</i> , 2017, 26, 5989-6001.	2.0	25
17	A Conifer UDP-Sugar Dependent Glycosyltransferase Contributes to Acetophenone Metabolism and Defense against Insects. <i>Plant Physiology</i> , 2017, 175, 641-651.	2.3	24
18	CNVs into the wild: screening the genomes of conifer trees (<i>Picea</i> spp.) reveals fewer gene copy number variations in hybrids and links to adaptation. <i>BMC Genomics</i> , 2017, 18, 97.	1.2	32

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19	Development of a Traceability System Based on a SNP Array for Large-Scale Production of High-Value White Spruce (<i>Picea glauca</i>). <i>Frontiers in Plant Science</i> , 2017, 8, 1264.	1.7	14
20	<i>In vivo</i> function of <i>Pgl2glu-1</i> in the release of acetophenones in white spruce. <i>PeerJ</i> , 2017, 5, e3535.	0.9	7
21	Dissection of expression quantitative trait locus and allele specificity using a haploid/diploid plant system – insights into compensatory evolution of transcriptional regulation within populations. <i>New Phytologist</i> , 2016, 211, 159-171.	3.5	28
22	Genetic architecture of wood properties based on association analysis and co-expression networks in white spruce. <i>New Phytologist</i> , 2016, 210, 240-255.	3.5	43
23	Conifer genomics and adaptation: at the crossroads of genetic diversity and genome function. <i>New Phytologist</i> , 2016, 209, 44-62.	3.5	73
24	Biochar and plant growth promoting rhizobacteria effects on switchgrass (<i>Panicum virgatum</i> cv.) and Bioenergy, 2016, 95, 167-173.	2.9	21
25	Improved white spruce (<i>Picea glauca</i>) genome assemblies and annotation of large gene families of conifer terpenoid and phenolic defense metabolism. <i>Plant Journal</i> , 2015, 83, 189-212.	2.8	200
26	Expression of the glucosidase gene <i>Pgl2glu1</i> underpins natural resistance of white spruce against spruce budworm. <i>Plant Journal</i> , 2015, 81, 68-80.	2.8	52
27	Forest Tree Genomics: Review of Progress. <i>Advances in Botanical Research</i> , 2015, 74, 39-92.	0.5	9
28	Modular organization of the white spruce (<i>Picea glauca</i>) transcriptome reveals functional organization and evolutionary signatures. <i>New Phytologist</i> , 2015, 207, 172-187.	3.5	35
29	From genotypes to phenotypes: expression levels of genes encompassing adaptive SNPs in black spruce. <i>Plant Cell Reports</i> , 2015, 34, 2111-2125.	2.8	5
30	Carbon dynamics in a biochar-amended loamy soil under switchgrass. <i>Canadian Journal of Soil Science</i> , 2015, 95, 1-13.	0.5	10
31	Identification of nitrogen responsive genes in poplar roots grown under two contrasting nitrogen levels. <i>Plant Root</i> , 2014, 8, 42-54.	0.3	2
32	Accuracy of genomic selection models in a large population of open-pollinated families in white spruce. <i>Heredity</i> , 2014, 113, 343-352.	1.2	127
33	What do ecological regions tell us about wood quality? A case study in eastern Canadian white spruce. <i>Canadian Journal of Forest Research</i> , 2014, 44, 1383-1393.	0.8	13
34	Genomic selection accuracies within and between environments and small breeding groups in white spruce. <i>BMC Genomics</i> , 2014, 15, 1048.	1.2	93
35	Opposite action of R2R3-MYBs from different subgroups on key genes of the shikimate and monolignol pathways in spruce. <i>Journal of Experimental Botany</i> , 2014, 65, 495-508.	2.4	34
36	Large-scale screening of transcription factor promoter interactions in spruce reveals a transcriptional network involved in vascular development. <i>Journal of Experimental Botany</i> , 2014, 65, 2319-2333.	2.4	59

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37	Insights into Conifer Giga-Genomes. <i>Plant Physiology</i> , 2014, 166, 1724-1732.	2.3	164
38	Evolution of gene structure in the conifer <i>Picea glauca</i> : a comparative analysis of the impact of intron size. <i>BMC Plant Biology</i> , 2014, 14, 95.	1.6	46
39	Potential link between biotic defense activation and recalcitrance to induction of somatic embryogenesis in shoot primordia from adult trees of white spruce (<i>Picea glauca</i>). <i>BMC Plant Biology</i> , 2013, 13, 116.	1.6	42
40	Differential gene expression patterns in white spruce newly formed tissue on board the International Space Station. <i>Advances in Space Research</i> , 2013, 52, 760-772.	1.2	12
41	Are long-lived trees poised for evolutionary change? Single locus effects in the evolution of gene expression networks in spruce. <i>Molecular Ecology</i> , 2013, 22, 2369-2379.	2.0	20
42	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584.	13.7	1,303
43	Assembling the 20 Gb white spruce (<i>Picea glauca</i>) genome from whole-genome shotgun sequencing data. <i>Bioinformatics</i> , 2013, 29, 1492-1497.	1.8	356
44	The Landscape of Nucleotide Polymorphism among 13,500 Genes of the Conifer <i>Picea glauca</i> , Relationships with Functions, and Comparison with <i>Medicago truncatula</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 1910-1925.	1.1	33
45	Development of high-density SNP genotyping arrays for white spruce (<i>Picea</i>) Tj ETQq1 1 0.784314 rgB 2013, 13, 324-336.	2.2	78
46	Genetic Improvement of White Spruce Mechanical Wood Traits—Early Screening by Means of Acoustic Velocity. <i>Forests</i> , 2013, 4, 575-594.	0.9	63
47	Towards decoding the conifer giga-genome. <i>Plant Molecular Biology</i> , 2012, 80, 555-569.	2.0	91
48	Can wood properties be predicted from the morphological traits of a tree? A canonical correlation study of plantation-grown white spruce. <i>Canadian Journal of Forest Research</i> , 2012, 42, 1518-1529.	0.8	16
49	Transcriptome profiling in conifers and the PiceaGenExpress database show patterns of diversification within gene families and interspecific conservation in vascular gene expression. <i>BMC Genomics</i> , 2012, 13, 434.	1.2	60
50	Association Genetics of Wood Physical Traits in the Conifer White Spruce and Relationships With Gene Expression. <i>Genetics</i> , 2011, 188, 197-214.	1.2	131
51	The influence of cambial age on breeding for wood properties in <i>Picea glauca</i> . <i>Tree Genetics and Genomes</i> , 2011, 7, 641-653.	0.6	30
52	Gene mapping in white spruce (<i>P. glauca</i>): QTL and association studies integrating population and expression data. <i>BMC Proceedings</i> , 2011, 5, .	1.8	2
53	Competing MYB networks as switches in primary and secondary metabolism in spruce. <i>BMC Proceedings</i> , 2011, 5, .	1.8	1
54	A White Spruce Gene Catalog for Conifer Genome Analyses. <i>Plant Physiology</i> , 2011, 157, 14-28.	2.3	143

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55	Molecular Evolution of Regulatory Genes in Spruces from Different Species and Continents: Heterogeneous Patterns of Linkage Disequilibrium and Selection but Correlated Recent Demographic Changes. <i>Journal of Molecular Evolution</i> , 2010, 70, 371-386.	0.8	40
56	Gene family structure, expression and functional analysis of HD-Zip III genes in angiosperm and gymnosperm forest trees. <i>BMC Plant Biology</i> , 2010, 10, 273.	1.6	39
57	<i>EgMYB1</i> , an R2R3 MYB transcription factor from eucalyptus negatively regulates secondary cell wall formation in <i>Arabidopsis</i> and poplar. <i>New Phytologist</i> , 2010, 188, 774-786.	3.5	180
58	High nitrogen fertilization and stem leaning have overlapping effects on wood formation in poplar but invoke largely distinct molecular pathways. <i>Tree Physiology</i> , 2010, 30, 1273-1289.	1.4	52
59	Subgroup 4 R2R3-MYBs in conifer trees: gene family expansion and contribution to the isoprenoid- and flavonoid-oriented responses. <i>Journal of Experimental Botany</i> , 2010, 61, 3847-3864.	2.4	146
60	Genetic control of wood properties in <i>Picea glauca</i> —an analysis of trends with cambial age. <i>Canadian Journal of Forest Research</i> , 2010, 40, 703-715.	0.8	82
61	SABATH methyltransferases from white spruce (<i>Picea glauca</i>): gene cloning, functional characterization and structural analysis. <i>Tree Physiology</i> , 2009, 29, 947-957.	1.4	20
62	Sequence analysis and functional characterization of the promoter of the <i>Picea glauca</i> Cinnamyl Alcohol Dehydrogenase gene in transgenic white spruce plants. <i>Plant Cell Reports</i> , 2009, 28, 787-800.	2.8	34
63	Evaluation of the impact of single nucleotide polymorphisms and primer mismatches on quantitative PCR. <i>BMC Biotechnology</i> , 2009, 9, 75.	1.7	73
64	Expression profiling and functional analysis of <i>Populus</i> WRKY23 reveals a regulatory role in defense. <i>New Phytologist</i> , 2009, 184, 48-70.	3.5	77
65	Identification of conserved core xylem gene sets: conifer cDNA microarray development, transcript profiling and computational analyses. <i>New Phytologist</i> , 2008, 180, 766-786.	3.5	87
66	Functional genomics of PycR, a LysR family transcriptional regulator essential for maintenance of <i>Pseudomonas aeruginosa</i> in the rat lung. <i>Microbiology (United Kingdom)</i> , 2008, 154, 2106-2118.	0.7	18
67	Involvement of <i>Pinus taeda</i> MYB1 and MYB8 in phenylpropanoid metabolism and secondary cell wall biogenesis: a comparative in planta analysis. <i>Journal of Experimental Botany</i> , 2008, 59, 3925-3939.	2.4	183
68	ForestTreeDB: a database dedicated to the mining of tree transcriptomes. <i>Nucleic Acids Research</i> , 2007, 35, D888-D894.	6.5	22
69	Molecular characterization of <i>EgMYB1</i> , a putative transcriptional repressor of the lignin biosynthetic pathway. <i>Plant Science</i> , 2007, 173, 542-549.	1.7	123
70	Genotypic variation in wood density and growth traits of poplar hybrids at four clonal trials. <i>Forest Ecology and Management</i> , 2007, 238, 92-106.	1.4	119
71	Diverse developmental mutants revealed in an activation-tagged population of poplar This article is one of a selection of papers published on the Special Issue of Poplar Research in Canada.. <i>Canadian Journal of Botany</i> , 2007, 85, 1071-1081.	1.2	31
72	Effects of Increased Nitrogen Supply on the Lignification of Poplar Wood. <i>Journal of Agricultural and Food Chemistry</i> , 2007, 55, 10306-10314.	2.4	64

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73	Conifer R2R3-MYB transcription factors: sequence analyses and gene expression in wood-forming tissues of white spruce (<i>Picea glauca</i>). <i>BMC Plant Biology</i> , 2007, 7, 17.	1.6	121
74	Short-term effects of nitrogen availability on wood formation and fibre properties in hybrid poplar. <i>Trees - Structure and Function</i> , 2007, 21, 249-259.	0.9	80
75	Genetic control of somatic embryogenesis initiation in loblolly pine and implications for breeding. <i>Tree Genetics and Genomes</i> , 2006, 2, 1-9.	0.6	66
76	Automated SNP detection from a large collection of white spruce expressed sequences: contributing factors and approaches for the categorization of SNPs. <i>BMC Genomics</i> , 2006, 7, 174.	1.2	68
77	Age trends in genotypic variation of wood density and its intra-ring components in young poplar hybrid crosses. <i>Annals of Forest Science</i> , 2006, 63, 673-685.	0.8	14
78	Generation, annotation, analysis and database integration of 16,500 white spruce EST clusters. <i>BMC Genomics</i> , 2005, 6, 144.	1.2	119
79	Large-scale statistical analysis of secondary xylem ESTs in pine. <i>Plant Molecular Biology</i> , 2005, 57, 203-224.	2.0	42
80	A robust neural networks approach for spatial and intensity-dependent normalization of cDNA microarray data. <i>Bioinformatics</i> , 2005, 21, 2674-2683.	1.8	35
81	Gene Expression during Formation of Earlywood and Latewood in Loblolly Pine: Expression Profiles of 350 Genes. <i>Plant Biology</i> , 2004, 6, 654-663.	1.8	47
82	Report on the Forest Trees Workshop at the Plant and Animal Genome Conference. <i>Comparative and Functional Genomics</i> , 2003, 4, 229-238.	2.0	10
83	Genes involved in the biosynthesis of lignin precursors in <i>Arabidopsis thaliana</i> . <i>Plant Physiology and Biochemistry</i> , 2003, 41, 677-687.	2.8	115
84	NMR analysis of lignins in CAD-deficient plants. Part 1. Incorporation of hydroxycinnamaldehydes and hydroxybenzaldehydes into lignins. <i>Organic and Biomolecular Chemistry</i> , 2003, 1, 268-281.	1.5	145
85	PULPING AND BLEACHING OF PARTIALLY CAD-DEFICIENT WOOD. <i>Journal of Wood Chemistry and Technology</i> , 2002, 22, 235-248.	0.9	16
86	Heterologous Array Analysis in Pinaceae: Hybridization of <i>Pinus taeda</i> cDNA Arrays with cDNA from Needles and Embryogenic Cultures of <i>P. taeda</i> , <i>P. sylvestris</i> or <i>Picea abies</i> . <i>Comparative and Functional Genomics</i> , 2002, 3, 306-318.	2.0	45
87	PULPING AND BLEACHING OF CAD-DEFICIENT WOOD. <i>Journal of Wood Chemistry and Technology</i> , 2001, 21, 1-17.	0.9	20
88	PYROLYSIS MASS SPECTRAL CHARACTERIZATION OF WOOD FROM CAD-DEFICIENT PINE. <i>Journal of Wood Chemistry and Technology</i> , 2001, 21, 19-29.	0.9	21
89	Elucidation of new structures in lignins of CAD- and COMT-deficient plants by NMR. <i>Phytochemistry</i> , 2001, 57, 993-1003.	1.4	195
90	Lignin Structure in a Mutant Pine Deficient in Cinnamyl Alcohol Dehydrogenase. <i>Journal of Agricultural and Food Chemistry</i> , 2000, 48, 2326-2331.	2.4	62

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91	Average effect of a mutation in lignin biosynthesis in loblolly pine. Theoretical and Applied Genetics, 1999, 99, 705-710.	1.8	43
92	Unexpected variation in lignin. Current Opinion in Plant Biology, 1999, 2, 145-152.	3.5	213
93	Modified Lignin and Delignification with a CAD-Deficient Loblolly Pine. Holzforschung, 1999, 53, 403-410.	0.9	35
94	Characterization of NAD-dependent mannitol dehydrogenase from celery as affected by ions, chelators, reducing agents and metabolites. Plant Science, 1998, 131, 43-51.	1.7	21
95	RECENT ADVANCES IN UNDERSTANDING LIGNIN BIOSYNTHESIS. Annual Review of Plant Biology, 1998, 49, 585-609.	14.2	404
96	Inheritance, gene expression, and lignin characterization in a mutant pine deficient in cinnamyl alcohol dehydrogenase. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 8255-8260.	3.3	194
97	Abnormal Lignin in a Loblolly Pine Mutant. Science, 1997, 277, 235-239.	6.0	311
98	Genetic analysis of cinnamyl alcohol dehydrogenase in loblolly pine: single gene inheritance, molecular characterization and evolution. Molecular Genetics and Genomics, 1995, 247, 537-545.	2.4	71